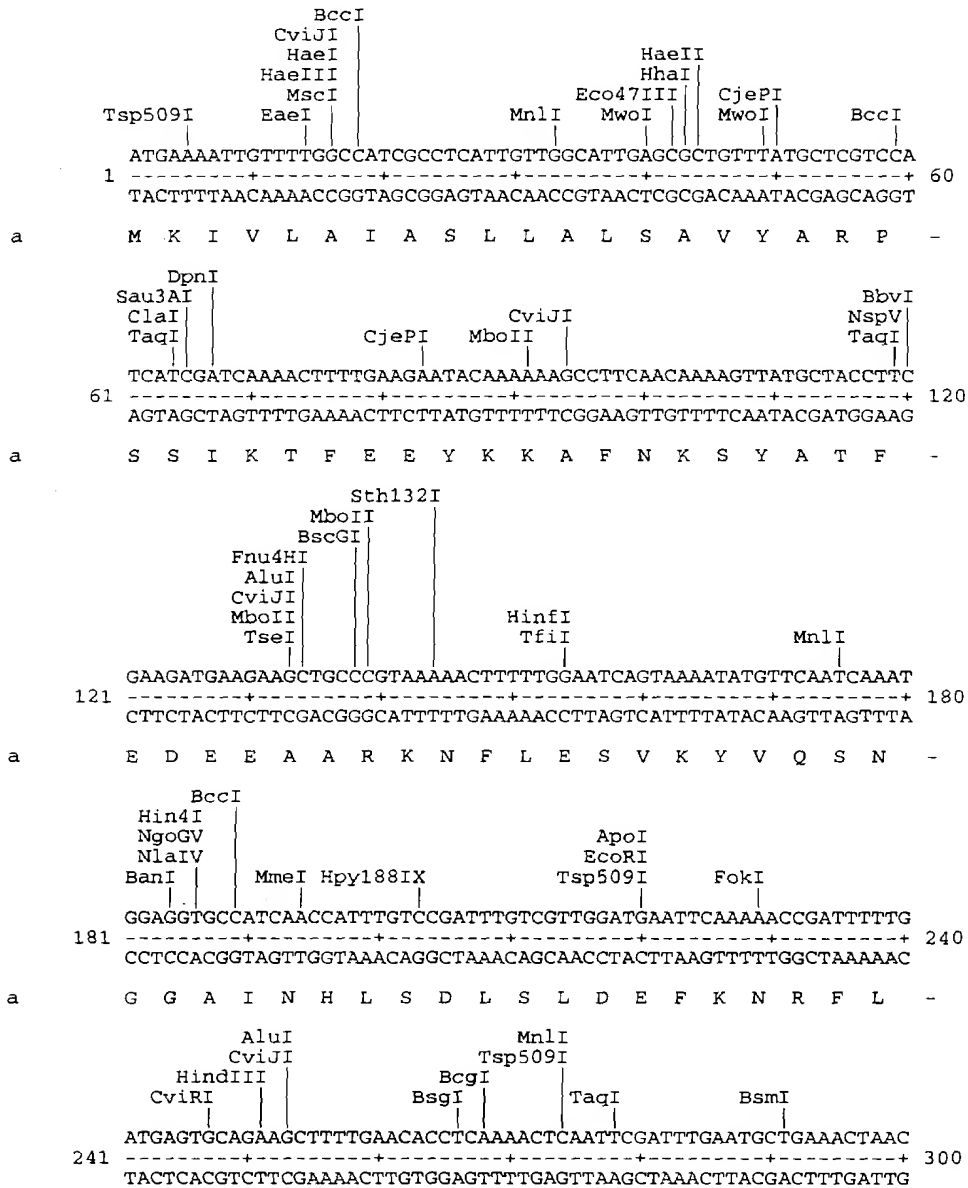


FIGURE 7: DerP1 restriction map of SEQ ID NO. 6.

(Linear) MAP of: Derp1.seq check: 7532 from: 1 to: 963

ID DP11695 standard; RNA; INV; 1099 BP.



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a M S A E A F E H L K T Q F D L N A E T N -
BpmI PstI BsaXI
CviRI AluI AclI
Cac8I CviJI MspAII ClaI MaeIII
SfcI PvuII TaqI MwoI Tsp45I
BcgI CjePI Tsp45I
GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTGCGACAAATGCGAACTGTC 360
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
a A C S I N G N A P A E I D L R Q M R T V -
CviRI MnlI NlaIII CviJI BsbI
MslI CviJI DrdII CviJI BsbI
ACTCCCATTCTGATGCAAGGAGGCTGTGGTTTCATGTTGGCTTTCTCTGGTGTGCGCA 420
TGAGGGTAAGCATACGTTCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT
a T P I R M Q G G C G S C W A F S G V A A -
HinFI AluI CviJI DpnI
TfiI CviJI MwoI TaaI BstYI Sau3AI AlwI Tsp509I
ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
a T E S A Y L A Y R N Q S L D L A E Q E L -
BsaAI FokI PmlI
TaqI BsbI TaaI NlaIII MaeII
CjeI HphI
GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATAACCATTCACGTTGTTGAATAC 540
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
a V D C A S Q H G C H G D T I P R G I E Y -
AluI MaeII BssSI
CjeI MslI CviJI ClaI CviRI
BstXI MmeI TaqI
ATCCAACATAATGGTGTGTCCTCAAGAAAGCTACTATCGATACGTTGCACGAGACAATCA 600
TAGGTTGTATTACCACAGCAGGTTCTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT
a I Q H N G V V Q E S Y Y R Y V A R E Q S -
NlaIII AclI ApoI
CviRI MaeII Tsp509I
CjeI
TGCCGACGACCAATGCACAACGTTTCGGTATCTCAAATATTGCCAAATTTACCCACCA 660
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGTGGT
a C R R P N A Q R F G I S N Y C Q I Y P P -

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```

                                     AluI
                                     CviJI
                                     CjeI
                                     HindIII
                                     Hpy178III
                                     ApoI
                                     Tsp509I
                                     CviJI
                                     BceI
                                     Eco47III
                                     HaeII
                                     HhaI
                                     RleAI
661  AATGTAACAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+-----+
a   N V N K I R E A L A Q T H S A I A V I I -

                                     CviJI
                                     HaeIII
                                     BccI
                                     EaeI
                                     GdiI
                                     SfaNI
                                     BsmI
                                     HgaI
                                     MslI
                                     ThaI
721  GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATCAACGCGAT 780
-----+-----+-----+-----+-----+-----+
a   G I K D L D A F R H Y D G R T I I Q R D -

BstEII
MaeIII
                                     HincII
                                     MaeIII
                                     TaaI
                                     DraIII
781  AATGGTTACCAACCAAACTATCACGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+
a   N G Y Q P N Y H A V N I V G Y S N A Q G -

                                     CjeI
                                     TaaI
                                     BciVI
                                     CjePI
                                     AlwI
                                     RsaI
                                     SunI
                                     DpnI
                                     Sau3AI
                                     TaqI
                                     HgiEII
                                     MunI
                                     Tsp509I
                                     MaeIII
                                     CjePI
                                     HphI
                                     BbvI
                                     TaaI
841  GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+
a   V D Y W I V R N S W D T N W G D N G Y G -

Fnu4HI
TseI
                                     ClaI
                                     TaqI
                                     Bsp24I
                                     CjePI
                                     CjeI
                                     MboII
                                     NdeI
901  TATTTTGCTGCCAACATCGATTGGATGATGATGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+
a   Y F A A N I D L M M I E E Y P Y V V I L -

TAA
961  --- 963
ATT
```

FIGURE 8: Sequence of full mutant DerP1 including pre-protein. Active site mutation Cys 132→Ala 132, corresponding to Cys34→Ala34 of the mature protein). Sequence includes coding (listed as SEQ ID NO. 6) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. 1).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAAACTTTTTGGAATCAGTAAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTGTCCGATTGTGCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAAACTCAATTCGATTTGAATGCTGAAACTAAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTGTGGAGTTTTGAGTTAAGCTAAACTTACGACTTTGATTG
M S A E A F E H L K T Q F D L N A E T N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCAGCTTGGGCTTTCTCTGGTGTGCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTCGAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S A W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```

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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCACGTGGTATTGAATAC 540
-----+-----+-----+-----+-----+-----+
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTCTGCCAAGAAAGCTACTATCGATACGTTGCACGAGAACAAATCA 600
-----+-----+-----+-----+-----+-----+
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660
-----+-----+-----+-----+-----+-----+
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCTGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+
TTACATTTGTTTTAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACCTATCACGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGATAGTGCGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA
N G Y Q P N Y H A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCCACTATTACCAATGCCA
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

ATT

FIGURE 9: Sequence of full mutant DerP1 including pre-protein containing a deletion at the propeptide cleavage site (NAET). Sequence includes coding (listed as SEQ ID NO. 7) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. 2).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACCTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAAACTTTTTGGAATCAGTAAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTGTGTCGATTGTGCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTG AAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTGTGGAGTTTTGAGTTAAGCTAAAC TTG
M S A E A F E H L K T Q F D L N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTGCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTACAACCCGAAAAGAGACCACAACGGCGT
T P I R M Q G G C G S C W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```

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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCACGTGGTATTGAATAC 540
-----+-----+-----+-----+-----+-----+-----+
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTCTGTCCTCAAGAAAGCTACTATCGATACGTTGCACGAGAACAAATCA 600
-----+-----+-----+-----+-----+-----+-----+
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTAGT
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660
-----+-----+-----+-----+-----+-----+-----+
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+-----+
TTACATTTGTTTTAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACCTATGCTGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGTAGTGCGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA
N G Y Q P N Y A A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCCACTATTACCAATGCCA
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

ATT

FIGURE 10: Sequence of full mutant DerP1 including pre-protein. Active site mutation His 268 → Ala 268, corresponding to His170→Ala170 of the mature protein). Sequence includes coding (listed as SEQ ID NO. 8) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. 3).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAACTTTTGAAGAAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAGAACTTCTTATGTTTTTCGGAAGTTGTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAACTTTTGGGAATCAGTAAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTGAAGAACTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCTGTTGGATGAATTCAAAAACCGATTTTGT 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTGAATGCTGAAACTAAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTTGTGGAGTTTGTAGTTAAGCTAACTTACGACTTTGATTG
M S A E A F E H L K T Q F D L N A E T N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTGCGGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S C W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```


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GTTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCACGTGGTATTGAATAC 540
-----+-----+-----+-----+-----+-----+-----+
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTCTGCCAAGAAAGCTACTATCGATACGTTGCACGAGAACAAATCA 600
-----+-----+-----+-----+-----+-----+-----+
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660
-----+-----+-----+-----+-----+-----+-----+
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720
-----+-----+-----+-----+-----+-----+-----+
TTACATTTGTTTAAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780
-----+-----+-----+-----+-----+-----+-----+
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACTAT**GCT**GCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840
-----+-----+-----+-----+-----+-----+-----+
TTACCAATGGTTGGTTTGATA**CGA**CGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA
N G Y Q P N Y A A V N I V G Y S N A Q G 280

GTTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900
-----+-----+-----+-----+-----+-----+-----+
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCCACTATTACCAATGCCA
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960
-----+-----+-----+-----+-----+-----+-----+
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

ATT

FIGURE 11: Amino acid sequence (SEQ ID NO: 4) for the mutant DerP1 as encoded by pNIV4842, and shown in figure 5.

1 MLLVNQSHQG FNKEHTSKMV SAIVLYVLLA AAAHSAFAAD PRPSSIKTFE
51 EYKKA FNKSY ATFEDEEAAR KNFLESVKYV QSNGGAINHL SDLSLDEFKN
101 RFLMSAEAFE HLKTQFDLNA CSINGNAPAE IDLRQMRTVT PIRMQGGCGS
151 CWA FSGVAAT ESAYLAYRNQ SLDLAEQELV DCASQHGCHG DTIPRGIEYI
201 QHNGVVQESY YRYVAREQSC RRPNAQRFGI SNYCQIYPPN ANKIREALAQ
251 THSAIAVIIG IKDLDAFRHY DGRTIIQRDN GYQPNYHAVN IVGYSNAQGV
301 DYWIVRNSWD TNWGDNGYGY FAANIDLMMI EEYPYVVIL*

FIGURE 12: Amino acid sequence (SEQ ID NO: 5) for the mutant DerP1 as encoded by pNIV4843, and shown in figure 6.

1 MLLVNQSHQG FNKEHTSKMV SAIVLYVLLA AAAHSAFAAD PRPSSIKTFE
51 EYKKAFNKSY ATFEDEEAAR KNFLESVKYV QSNNGGAINHL SDLSLDEFKN
101 RFLMSAEAFE HLKTQFDLNA ETNACSINGN APAEIDLRQM RTVTPIRMQG
151 GCGSAWAFSG VAATESAYLA YRNQSLDLAE QELVDCASQH GCHGDTIPRG
201 IEYIQHNGVV QESYYRYVAR EQSCRRPNAQ RFGISNYCQI YPPNANKIRE
251 ALAQTHSAIA VIIGIKDLDA FRHYDGRTII QRDNGYQPNY HAVNIVGYSN
301 AQGVVDYWIVR NSWDTNWGDN GYGYFAANID LMMIEEYPYV VIL*